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TECH CENTER 1600/2900 1652 1600

RAW SEQUENCE LISTING   DATE: 12/20/2001
PATENT APPLICATION: US/09/246,451A   TIME: 08:56:29

        Input Set : **A:\Seqlist.txt**
        Output Set: **N:\CRF3\12192001\I246451A.raw**

ENTERED

Updated
RSL

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  4 <110> APPLICANT: California Institute of Technology;
  5         Frances H. Arnold
  6         Hyun Joo
  8 <120> TITLE OF INVENTION: Oxygenase Enzymes and Screening Method
 11 <130> FILE REFERENCE: 9373/1E827-US1
 13 <140> CURRENT APPLICATION NUMBER: US 09/246,451A
C--> 14 <141> CURRENT FILING DATE: 1999-02-09
 16 <150> PRIOR APPLICATION NUMBER: US 60/094,403
 17 <151> PRIOR FILING DATE: 1998-07-28
 19 <150> PRIOR APPLICATION NUMBER: US 60/106,840
 20 <151> PRIOR FILING DATE: 1998-11-03
 22 <150> PRIOR APPLICATION NUMBER: US 60/086,206
 23 <151> PRIOR FILING DATE: 1998-05-21
 25 <150> PRIOR APPLICATION NUMBER: US 60/106,834
 26 <151> PRIOR FILING DATE: 1998-11-03
 28 <160> NUMBER OF SEQ ID NOS: 19
 30 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 1402
 34 <212> TYPE: DNA
 35 <213> ORGANISM: P. Putida
 37 <400> SEQUENCE: 1
 38  ctgcaggatc gttatccgct ggccgatctg atcacccagc gttttttccat cgacgaggcc      60
 39  agcaaggcac ttgaactggt caaggcagga gcactgatca aacccgtgat cgactccact     120
 40  ctttagccaa cccgcgttcc aggagaacaa caacaatgac gactgaaacc atacaaagca     180
 41  acgccaatct tgcccctctg ccaccccatg tgccagagca cctggtattc gacttcgaca     240
 42  tgtacaatcc gtcgaatctg tctgccggcg tgcaggaggc ctgggcagtt ctgcaagaat     300
 43  caaacgtacc ggatctggtg tggactcgct gcaacggcgg acactggatc gccactcgcg     360
 44  gccaactgat ccgtgaggcc tatgaagatt accgccactt ttccagcgag tgcccgttca     420
 45  tccctcgtga agccggcgaa gcctacgact tcattcccac ctcgatggat ccgcccgagc     480
 46  agcgccagtt tcgtgcgctg gccaaccaag tggttggcat gccggtggtg gataagctgg     540
 47  agaaccggat ccaggagctg gcctgctcgc tgatcgagag cctgcgcccg caaggacagt     600
 48  gcaacttcac cgaggactac gccgaaccct tcccgatacg catcttcatg ctgctcgcag     660
 49  gtctaccgga agaagatatc ccgcacttga aatacctaac ggatcagatc acccgtccgg     720
 50  atggcagcat gaccttcgca gaggccaagg aggcgctcta cgactatctg ataccgatca     780
 51  tcgagcaacg caggcagaag ccgggaaccg acgctatcag catcgttgcc aacggccagg     840
 52  tcaatgggcg accgatcacc agtgacgaag ccaagaggat gtgtggcctg ttactggtcg     900
 53  gcggcctgga tacggtggtc aatttcctca gcttcagcat ggagttcctg gccaaaagcc     960
 54  cggagcatcg ccaggagctg atcgagcgtc ccgagcgtat ccagccgct tgcgaggaac    1020
 55  tactccggcg cttctcgctg gttgccgatg ccgcatcct cacctccgat tacgagtttc    1080
 56  atggcgtgca actgaagaaa ggtgaccaga tcctgctacc gcagatgctg tctggcctgg    1140
 57  atgagcgcga aaacgcctgc ccgatgcacg tcgacttcag tcgccaaaag gtttcacaca    1200
 58  ccacctttgg ccacggcagc catctgtgcc ttggccagca cctggcccgc cgggaaatca    1260
 59  tcgtcaccct caaggaatgg ctgaccagga ttcctgactt ctccattgcc ccgggtgccc    1320
 60  agattcagca caagagcggc atcgtcagcg gcgtgcaggc actccctctg gtctgggatc    1380
 61  cggcgactac caaagcggta ta                                            1402
 63 <210> SEQ ID NO: 2
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64 <211> LENGTH: 414
65 <212> TYPE: PRT
66 <213> ORGANISM: P. Putida
68 <400> SEQUENCE: 2
69   Thr Thr Glu Thr Ile Gln Ser Asn Ala Asn Leu Ala Pro Leu Pro Pro
70   1               5                  10                 15
71   His Val Pro Glu His Leu Val Phe Asp Phe Asp Met Tyr Asn Pro Ser
72               20                  25                 30
73   Asn Leu Ser Ala Gly Val Gln Glu Ala Trp Ala Val Leu Gln Glu Ser
74           35                  40                  45
75   Asn Val Pro Asp Leu Val Trp Thr Arg Cys Asn Gly Gly His Trp Ile
76       50                  55                  60
77   Ala Thr Arg Gly Gln Leu Ile Arg Glu Ala Tyr Glu Asp Tyr Arg His
78   65                  70                  75                  80
79   Phe Ser Ser Glu Cys Pro Phe Ile Pro Arg Glu Ala Gly Glu Ala Tyr
80                   85                  90                  95
81   Asp Phe Ile Pro Thr Ser Met Asp Pro Pro Glu Gln Arg Gln Phe Arg
82               100                 105                 110
83   Ala Leu Ala Asn Gln Val Val Gly Met Pro Val Val Asp Lys Leu Glu
84               115                 120                 125
85   Asn Arg Ile Gln Glu Leu Ala Cys Ser Leu Ile Glu Ser Leu Arg Pro
86       130                 135                 140
87   Gln Gly Gln Cys Asn Phe Thr Glu Asp Tyr Ala Glu Pro Phe Pro Ile
88   145                 150                 155                 160
89   Arg Ile Phe Met Leu Leu Ala Gly Leu Pro Glu Glu Asp Ile Pro His
90               165                 170                 175
91   Leu Lys Tyr Leu Thr Asp Gln Met Thr Arg Pro Asp Gly Ser Met Thr
92               180                 185                 190
93   Phe Ala Glu Ala Lys Glu Ala Leu Tyr Asp Tyr Leu Ile Pro Ile Ile
94               195                 200                 205
95   Glu Gln Arg Arg Gln Lys Pro Gly Thr Asp Ala Ile Ser Ile Val Ala
96       210                 215                 220
97   Asn Gly Gln Val Asn Gly Arg Pro Ile Thr Ser Asp Glu Ala Lys Arg
98   225                 230                 235                 240
99   Met Cys Gly Leu Leu Leu Val Gly Gly Leu Asp Thr Val Val Asn Phe
100              245                 250                 255
101  Leu Ser Phe Ser Met Glu Phe Leu Ala Lys Ser Pro Glu His Arg Gln
102              260                 265                 270
103  Glu Leu Ile Glu Arg Pro Glu Arg Ile Pro Ala Ala Cys Glu Glu Leu
104              275                 280                 285
105  Leu Arg Arg Phe Ser Leu Val Ala Asp Gly Arg Ile Leu Thr Ser Asp
106      290                 295                 300
107  Tyr Glu Phe His Gly Val Gln Leu Lys Lys Gly Asp Gln Ile Leu Leu
108  305                 310                 315                 320
109  Pro Gln Met Leu Ser Gly Leu Asp Glu Arg Glu Asn Ala Cys Pro Met
110              325                 330                 335
111  His Val Asp Phe Ser Arg Gln Lys Val Ser His Thr Thr Phe Gly His
112              340                 345                 350
113  Gly Ser His Leu Cys Leu Gly Gln His Leu Ala Arg Arg Glu Ile Ile
```

```
114          355                 360                365
115  Val Thr Leu Lys Glu Trp Leu Thr Arg Ile Pro Asp Phe Ser Ile Ala
116      370                 375                380
117  Pro Gly Ala Gln Ile Gln His Lys Ser Gly Ile Val Ser Gly Val Gln
118  385                 390                395                400
119  Ala Leu Pro Leu Val Trp Asp Pro Ala Thr Thr Lys Ala Val
120                  405                 410
122  <210> SEQ ID NO: 3
123  <211> LENGTH: 31
124  <212> TYPE: DNA
125  <213> ORGANISM: Artificial Sequence
127  <220> FEATURE:
128  <223> OTHER INFORMATION: Primer sequence
130  <400> SEQUENCE: 3
131   gatcatgaat gagaccgaca catcacctat c                              31
133  <210> SEQ ID NO: 4
134  <211> LENGTH: 32
135  <212> TYPE: DNA
136  <213> ORGANISM: Artificial Sequence
138  <220> FEATURE:
139  <223> OTHER INFORMATION: Primer sequence
141  <400> SEQUENCE: 4
142   acgaattcta gaagaagaaa ctgaggttat tg                             32
144  <210> SEQ ID NO: 5
145  <211> LENGTH: 27
146  <212> TYPE: DNA
147  <213> ORGANISM: Artificial Sequence
149  <220> FEATURE:
150  <223> OTHER INFORMATION: Primer sequence
152  <400> SEQUENCE: 5
153   ttggatccgg tggaccttgt ccatttg                                   27
155  <210> SEQ ID NO: 6
156  <211> LENGTH: 29
157  <212> TYPE: DNA
158  <213> ORGANISM: Artificial Sequence
160  <220> FEATURE:
161  <223> OTHER INFORMATION: Primer sequence
163  <400> SEQUENCE: 6
164   gctctagatc aaccgaagtg cttgtcgag                                 29
166  <210> SEQ ID NO: 7
167  <211> LENGTH: 24
168  <212> TYPE: DNA
169  <213> ORGANISM: Artificial Sequence
171  <220> FEATURE:
172  <223> OTHER INFORMATION: Primer sequence
174  <400> SEQUENCE: 7
175   cggaattcta ggaaacagac catg                                      24
177  <210> SEQ ID NO: 8
178  <211> LENGTH: 29
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179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: Primer sequence
185 <400> SEQUENCE: 8
186   ccggatccaa cctgggtcga agtcaaatg                              29
188 <210> SEQ ID NO: 9
189 <211> LENGTH: 24
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Primer sequence
196 <400> SEQUENCE: 9
197   catcgatgct taggaggtca tatg                                  24
199 <210> SEQ ID NO: 10
200 <211> LENGTH: 25
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence
204 <220> FEATURE:
205 <223> OTHER INFORMATION: Primer sequence
207 <400> SEQUENCE: 10
208   tcatgtttga cagcttatca tcgat                                 25
210 <210> SEQ ID NO: 11
211 <211> LENGTH: 414
212 <212> TYPE: PRT
213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Mutant M7-4H
218 <400> SEQUENCE: 11
219 Thr Thr Glu Thr Ile Gln Ser Asn Ala Asn Leu Ala Pro Leu Pro Pro
220 1               5                   10                  15
221 His Val Pro Glu His Leu Val Phe Asp Phe Asp Met Tyr Asn Pro Ser
222             20                  25                  30
223 Asn Leu Ser Ala Gly Val Gln Glu Ala Trp Ala Val Leu Gln Glu Ser
224         35                  40                  45
225 Asn Val Pro Asp Leu Val Trp Thr Arg Cys Asn Gly Gly His Trp Ile
226     50                  55                  60
227 Ala Thr Arg Gly Gln Leu Ile Arg Glu Ala Tyr Glu Asp Tyr Arg His
228 65                  70                  75                  80
229 Phe Ser Ser Glu Cys Pro Phe Ile Pro Arg Glu Ala Gly Glu Ala Tyr
230             85                  90                  95
231 Asp Phe Ile Pro Thr Ser Met Asp Pro Pro Glu Gln Arg Gln Phe Arg
232             100                 105                 110
233 Ala Leu Ala Asn Gln Val Val Gly Met Pro Val Val Asp Lys Leu Glu
234         115                 120                 125
235 Asn Arg Ile Gln Glu Leu Ala Cys Ser Leu Ile Glu Ser Leu Arg Pro
236     130                 135                 140
237 Gln Gly Gln Cys Asn Phe Thr Glu Asp Tyr Ala Glu Pro Phe Pro Ile
238 145                 150                 155                 160
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239  Arg Ile Phe Met Leu Leu Ala Gly Leu Pro Glu Glu Asp Ile Pro His
240              165             170             175
241  Leu Lys Tyr Leu Thr Asp Gln Met Thr Arg Pro Asp Gly Ser Met Thr
242              180             185             190
243  Phe Ala Glu Ala Lys Glu Ala Leu Tyr Asp Tyr Leu Ile Pro Ile Ile
244              195             200             205
245  Glu Gln Arg Arg Gln Lys Pro Gly Thr Asp Ala Ile Ser Ile Val Ala
246       210             215             220
247  Asn Gly Gln Val Asn Gly Arg Pro Ile Thr Ser Asp Glu Ala Lys Arg
248  225             230             235             240
249  Met Cys Gly Leu Leu Leu Val Gly Gly Leu Asp Thr Val Val Asn Phe
250              245             250             255
251  Leu Ser Phe Ser Met Glu Phe Leu Ala Lys Ser Pro Glu His Arg Gln
252              260             265             270
253  Glu Leu Ile Glu Arg Pro Glu Arg Ile Pro Ala Ala Cys Glu Glu Leu
254              275             280             285
255  Leu Arg Arg Phe Ser Leu Val Ala Asp Gly Arg Ile Leu Thr Ser Asp
256       290             295             300
257  Tyr Glu Phe His Gly Val Gln Leu Lys Lys Gly Asp Gln Ile Leu Leu
258  305             310             315             320
259  Pro Gln Met Leu Ser Gly Leu Asp Glu Arg Lys Asn Ala Cys Pro Met
260              325             330             335
261  His Val Asp Phe Ser Arg Gln Lys Val Ser His Thr Thr Phe Gly His
262              340             345             350
263  Gly Ser His Leu Cys Leu Gly Gln His Leu Ala Arg Arg Glu Ile Ile
264              355             360             365
265  Val Thr Leu Lys Glu Trp Leu Thr Arg Ile Pro Asp Phe Ser Ile Ala
266       370             375             380
267  Pro Gly Ala Gln Ile Gln His Lys Ser Gly Ile Val Ser Gly Val Gln
268  385             390             395             400
269  Ala Leu Pro Leu Val Trp Asp Pro Ala Thr Thr Lys Ala Val
270              405             410
272  <210> SEQ ID NO: 12
273  <211> LENGTH: 414
274  <212> TYPE: PRT
275  <213> ORGANISM: Artificial Sequence
277  <220> FEATURE:
278  <223> OTHER INFORMATION: Mutant M7-6H
280  <400> SEQUENCE: 12
281  Thr Thr Glu Thr Ile Gln Ser Asn Ala Asn Leu Ala Pro Leu Pro Pro
282   1               5               10              15
283  His Val Pro Glu His Leu Val Phe Asp Phe Asp Met Tyr Asn Pro Ser
284              20              25              30
285  Asn Leu Ser Ala Gly Val Gln Glu Ala Trp Ala Val Leu Gln Glu Ser
286              35              40              45
287  Asn Val Pro Asp Leu Val Trp Thr Arg Cys Asn Gly Gly His Trp Ile
288       50              55              60
289  Ala Thr Arg Gly Gln Leu Ile Arg Glu Ala Tyr Glu Asp Tyr Arg His
290  65              70              75              80
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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date